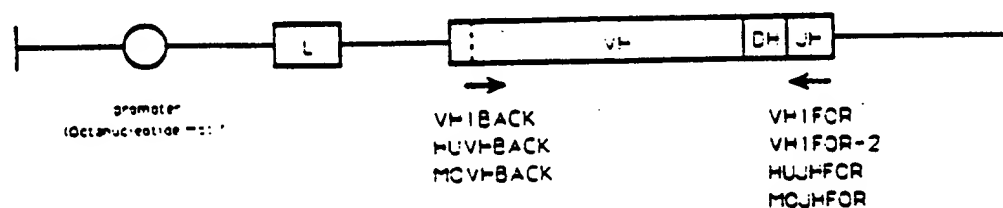
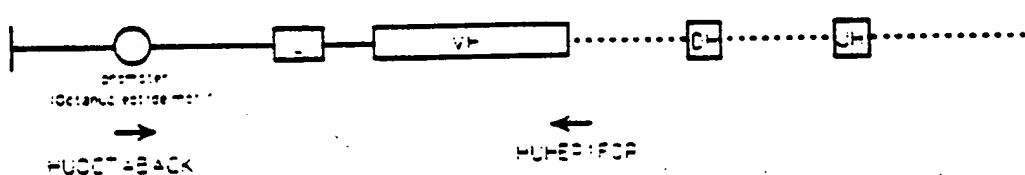


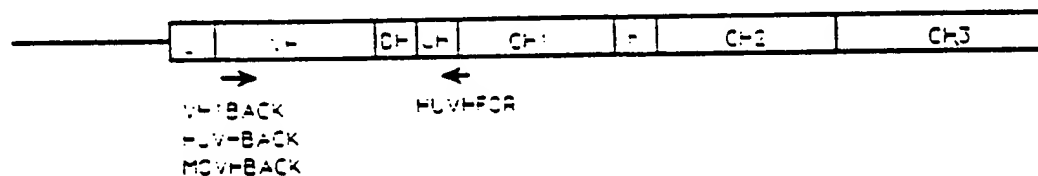
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

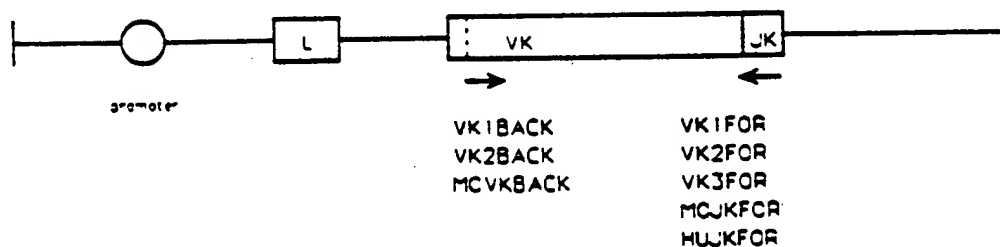


FIG. 1

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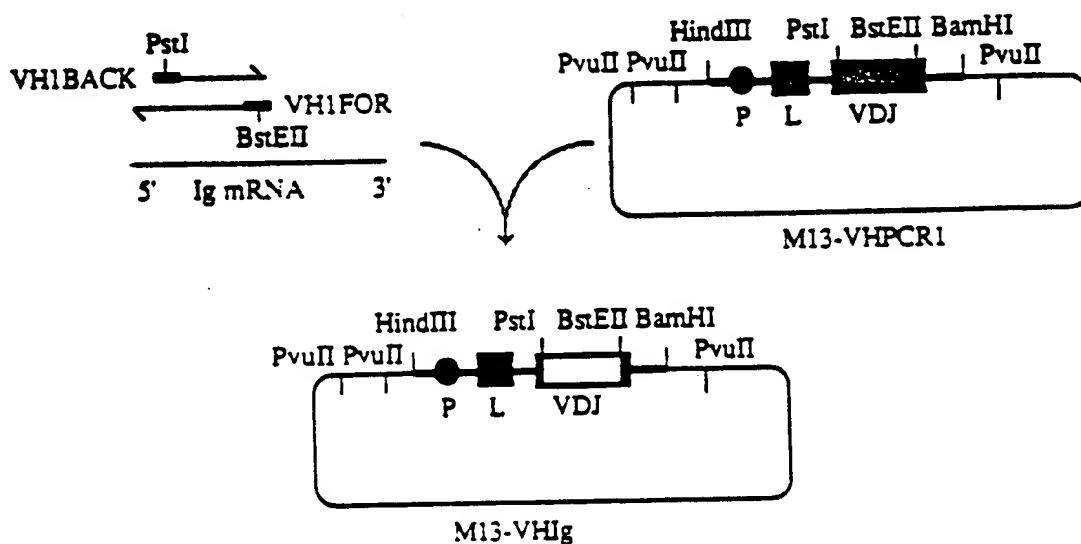


FIG. 2

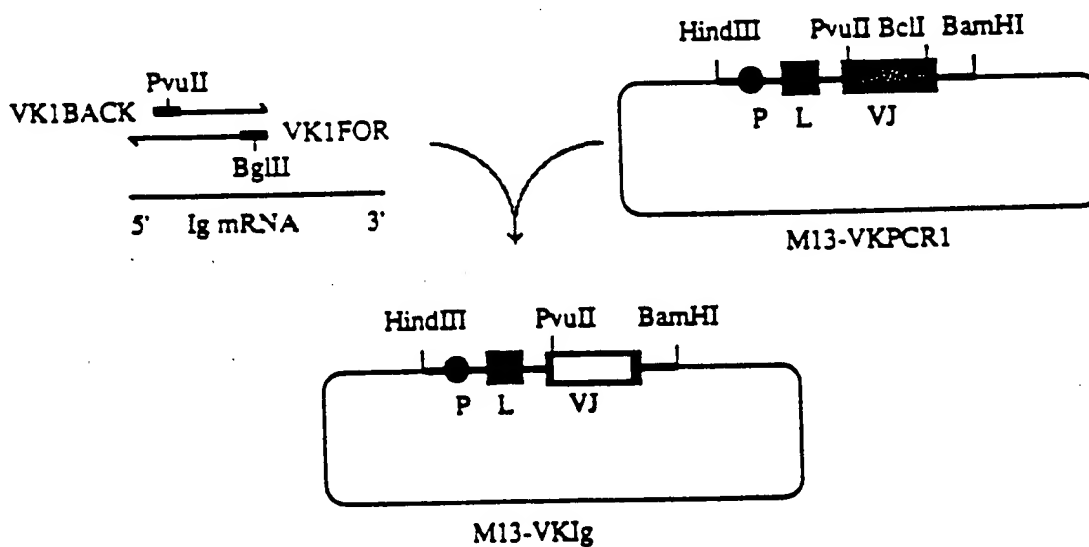


FIG. 4

00327-492260

HLA-III (1)

AAG TAT GAA TGC AA TCT CTG ATC AC TGG TAA TAT AGG TTG CTA TAC CA

CAACGAAAAACATGAGTACAGTTTCTTACAGTTACTGAGACACAGGACCTAC
70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTTCTATACCTCTTTTGGTAGCAACAGCTACAGGTAGGGGGCTCAC
130 140 150 160 170 180

AGTAGGAGCCTGAGCTTGGACATATATGGTGCATGCATCCACTTTGCCCTTC
190 200 210 220 230 240

PstI
 51
 10
 G V H S Q V Q L Q E S G P G L V R P
 TTTTACAGGTTTTCACATGAGTTCACAGGAGCGTCCAGGTGTGTGAGAC
 250 255 270 280 290 300

CDR1

15 20 25 30
S Q T L S L T C T V S G S T F S S Y W M

CTAGCCAGACCGCTGAGCTGACCTGACCTGACCTGCTGTCGACGACCTTCAGCAGCTACTGGA

310 320 330 340 350 360

CDR2

35 40 45 50
H W V R Q P P G R G L E W I G R I D P N
TGCAGTGGGTGAGACAGCCACCTGGAGCGAGTCTTGAGTGGATTGGAAGGATTGATCTCTA
370 380 390 400 410 420

55 60 65 70
S G G T K Y N E K F K S R V T M L V D T
ATAGTGGTGGTACTAGTACAATGAGAGAGTTCAAGAGCAGAGTGACAATGCTGGTAGACA
430 440 450 460 470 480

75 80 85 90
 S K N G F S L R L S S V T A A D T A V Y
 CGAGCAGAACCGATTGACCTGAGACTGACAGCGGTGACAGCGCCGACACCGGGTCT
 490 500 510 520 530 540

CDR3

95 100 105 110
Y C A R Y D Y Y G S S Y F D Y W G Q G T
ATTATTGTGCAAGATACCACTACTACGGTACTAGCTACTTTGACTACTGGGGCAAGGGA
550 560 570 580 590 600

BstEII
 115 | 120
 T V T V S S
 CCACGATACCGCTCTCTCTCAGGTGAGTGCCTTACAACGCTCTCTCTCTATTGAGCTTAAAT
 610 620 630 640 650 660

AGATTCTACTGCAATTTGTTGGGGGGAAATGTGTGTATCTGAATTCAGGTCAATGAAGGA
670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGGTCATTGGGAGCCCGGGCTGATGCAGACAGACA
730 740 750 760 770 780

BamHI

TCTCAGCTCCAGACTTCTATGCCAGAGATTATAG
 790 810 820

FIG. 3

003344

ML3_VkPCR1

Hand 222

[illegible]

CAAACAGAAAACATGAGATCACAGTTTCTTTACGTTACTGAGGCACAGGACCTCAC
 98 108 118 128 138 148

M G W S C I I I F L V A T A T
 CATGGGAGGAGCTGATACAGAGGCTTTTCTATGACAGCTACAGTAAAGGGGCTCAC
 158 168 178 188 198 208

AGTAGCAGGCTTGAGGTCGGACATATATGGTTACCATGACATCGACTTGGCTTTC
218 228 238 248 258 268

25 22

G V H S D : Q L : Q S P S S L S A S
 TTTCCAGAGTGTCTACTTGGACATTTCTGCTTCTCAGGCCCTAGCGGCTGAGCGCCA
 273 285 297 309 318 328

15 25 35 45 55 65 75 85 95 105 115 125 135 145 155 165 175 185 195 205 215 225 235 245 255 265 275 285 295 305 315 325 335 345 355 365 375 385 395 405 415 425 435 445 455 465 475 485 495 505 515 525 535 545 555 565 575 585 595 605 615 625 635 645 655 665 675 685 695 705 715 725 735 745 755 765 775 785 795 805 815 825 835 845 855 865 875 885 895 905 915 925 935 945 955 965 975 985 995
 V G D R V I T C R A S G N I H N Y L A
 GCTGGGTGCACAGCTGACGATCCTGCTTATGACGAGCGGTACATTCACAACTACCTGG
 138 345 352 368 378 388

CDR2

35 40 45 50
W Y Q Q K P G K A F K L L T Y T T T L
CTTGGTACCAACAGAACCGAGGTAAAGGCTGCAAGTCTGATCTACTACCAACCACCCC
398 408 418 428 438 448

5: 60 6: 70
A C G V P S R F S G S G S G T D F T F T
TGGCTACGGTGTGCCAAGCAGATTACGGGTACCGTACGGGTACCGACTTCACCTTCA
458 468 478 488 498 508

CDR3

75 80 85 90

I S S L Q P E D I A T Y Y C Q H F W S T

CCATCAGCAGCCTCCAGGCAGAGGACATCGCCACCTACTACTGCCAGCAGCTTCTGGAGCA

518 528 538 548 558 568

Bcl I (requires dam⁻ host)

95 100 105 108
 P R T F G Q G T K V V I K R
 CCCCAGGACGTCGGGCAAGGGACCAAGTGGGATCAACGTCAGTAGAATTAAAC
 578 589 598 608 618 628

පිළිගැනීම

628 348

FIG. 5

BOOK REVIEW

Sequence of MBr1 VH

Splice -1
↓ G V H S
AGGTGTCACCTCC

1 Pst- 10 20

Q V Q L E S G T E L A S P G A S V T L
CAGGTGGCACTGCGCAGTGAATGAACTGACTGAGCTGGCGAGTCCTGGGGCATCAGTGACACTG

VHIBACK SITE

30 CDR1 40

S C K A S' G Y T F T [D H I N] W V K K R
TCCTGCCAAGGCCTTCTGGCTACACATTACTGACCATAATTATAAATGGTAAAAAAGAGG

52a 53 CDR2

P G Q G L E W I G [R I Y P V S G V T N Y]
CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTTATCCAGTAAGTGGTGAACATAACTAC

50 65 70

[N C K F M E] K A T F S V D R S S N T V Y
AATCAAAAATTCATGGGCAAGGGCACATTTCTGTGAGACCGGTCTTCCAACACAGTGTAC

80 82a B C 83 90 CDR3

M V L N S L T S E D P A V Y Y C G R G [G F]
ATGTGTGTGAACAGTGTGACATGTGAGGACCGGTGCTGTCTATTACTGTGGAAGGGGCTT

HSP2 103 BstEII Splice

[E F D Y] W G Q G T T V T V S S ↓
GATTTTGACTACTTGGGGCCAGGGGACCACGGTACCGTCTCTCAGG.....

VHIFOR SITE

Sequence of MB-1 VK

Splice -1
↓ G V H S
AGGTGTCCACTCC
20

1 PvuII 10
D : Q L T Q S P P S L T V S V G E R V T
GAGATTAGGTTGGGAGTTTTCCCATCCCTGACTGTGTCACTAGGAGAGAGGGTCACT
VKIBACK SITE

27A B C D E F CDR1
I S C K S N C N L L W S G N R R Y C L G
ATCAGTTTGCAAATCCCAATCAGATCTTTTATGGAGTGGAAACCGAAGGTACTGTITGGGG
35 40 50 CDR2
W H Q W K P G Q T P T P L I T W T S D R
TGGCACCAGTGGAAACCGAGGGGCAAACCTCCTACACCGTTGATCACCTGGAGCATCTGATAGG
60 70
F S G V P D R F I G S G S V T D F T L T
TTCTCTGGAGTCCCTGATCGTTTCATAGGCGAGTGGATCTGTGACAGATTTCACCTGTGACC
80 90 CDR3
I S S V Q A E D V A V Y F C Q Q H L D L
ATCAGCAGTGTGACGGGTGAAGATGTGGCAGTTTATTCTGTGACGAACATTTGGAGCTT
95 100 BglII/BclI Splice
P Y T F G G G T K L E I K ↓
CCGTACACGTTCCGAGGGGGGACCAAGCTGGAGATCAAACGTGAG
VKIFOR SITE

FIG. 6

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α -Lys 30

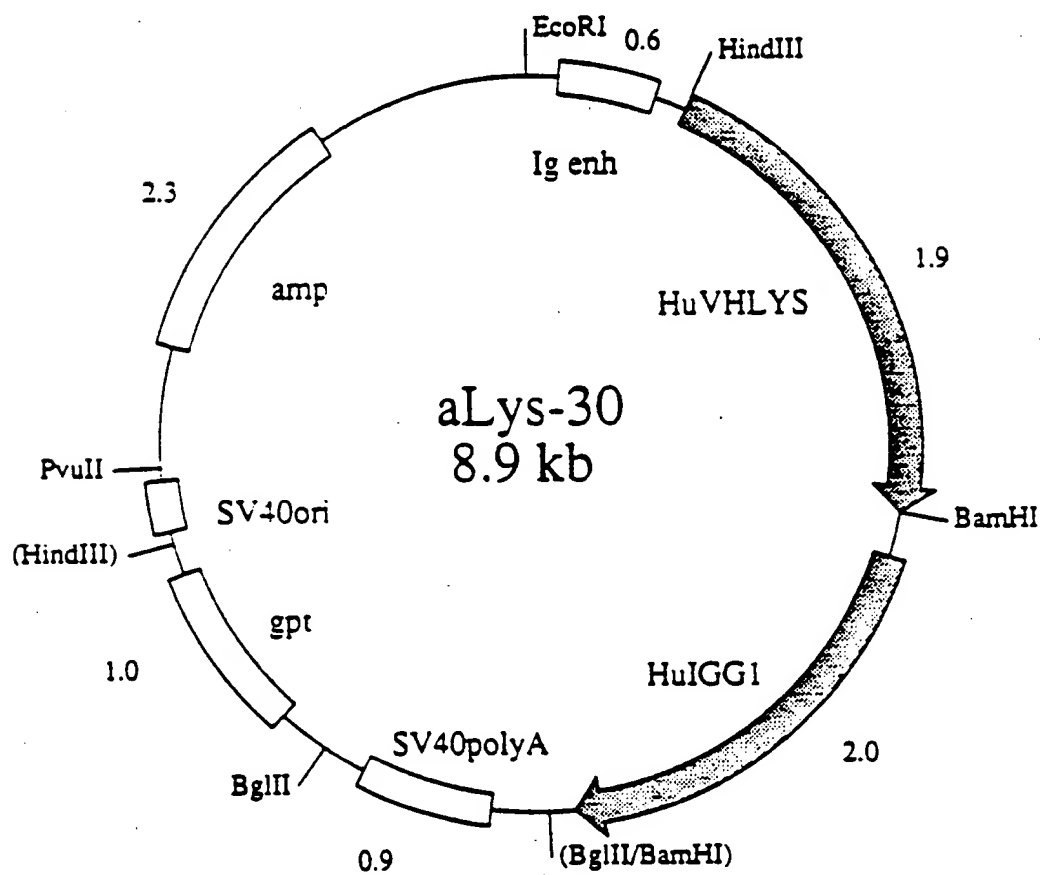


FIG. 7

α -Lys 17

7/23

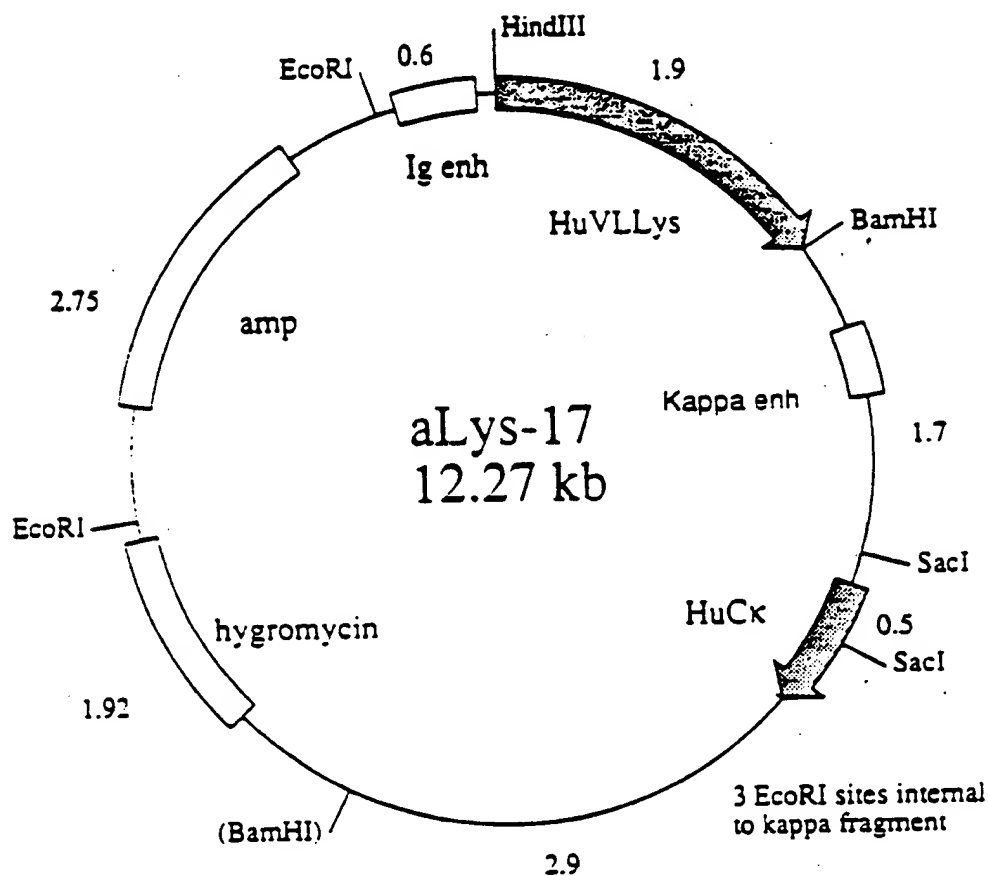


FIG. 8

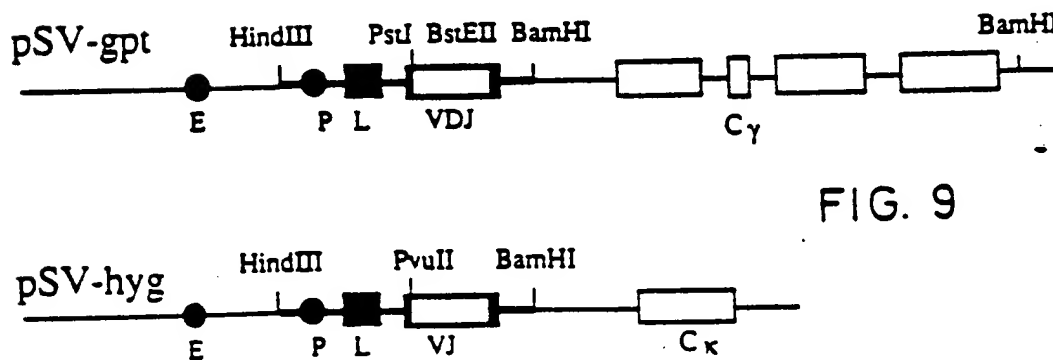


FIG. 9

ZENWZFAV
 DRXKLGFWFAV
 DSSGSWVY
 VSSGYISWVY

HESSSYTAY
 HESSY
 HESYANDY
 KREYDERGYYYANDY
 YYDSFFAY
 ESYFFAY
 YYDESSYYANDY
 11 22.
 21 22.
 29 22.
 17 22.
 32 22.

7s.gene/Unproductive
Unproductive
Unproductive
Unproductive
Unproductive

Figure 6

Unproductive
Unproductive

RELTYVACY
 VYVYVYVY
 PNYVYVYVYVYVYVY
 VYVYVYVY
 SSGYVY
 GAARATVYVY
 GGFYVY
 SPYVY
 EYVYVYVYVYVYVY
 VYVYVYVYVYVYVYVY
 EYVYVYVY
 KGYVYVYVYVYVYVY
 GYVYVYVY
 24 00.
 9 00.
 23 00.
 15 00.
 15 00.

Ps.gene
Ps.gene/Unproductive
Unproductive
Unproductive
Unproductive

WMLGAMV
GYYVCGSYVAMV
23 02.

Unproductive

AKHLYEDY
RECVESRLOGOV
RGLHWDFP
RNYGSSPFY
PPMPSY
43 02.
28 02.
15 02.

Ps.gene
Ps.gene
Ps.gene
Ps.gene
Ps.gene/Unproductive
Ps.gene/Unproductive
Unproductive

3C 22.

Unproductive

RECEIVED:

FIG. 10b

0 9 5 1 2 3 4 5 6 7 8 9
 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 103

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CDR 2FRAMWORK 3CDR 3

KABAT HUMAN VH1

	STSTAYMELRSLRSEDVAVYCAR	GEGWQHFDY
HACKFQG	RVTIRRHKSTSTAYMELSSLRSEDVAVYCAR	GSRYGYDCSGYYL
GYACKFQG	RVTMRRTSTSTAYMELSSLRSEDVAVYCAR	LAHFGSGSPVDWDF

KABAT HUMAN VH2

KHQLQPSLKS	RVTISVDTSKNQFSLKLSSTAAOTAVYYCAR	GGVWPAAIMDV
KS	RVTISVDTSKNQFSLKLSSTAAOTAVYYCAR	MARYYDFWSGYSAYDY
SLKS	RLSISQDTSPNQFSLRLSSTAAOTAVYYCAR	HRNWGSPVHFDY
	ESTSTAYMELSSLRSEDVAVYCAR	DSYGQYGGHY

KABAT HUMAN VH3

ISYITSSSSYNYADSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLVNLSLKTEDTAVYYCTR	TIYYDSSSGYPYW
YADSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	GIALDAFDI
YYADSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	53 NT. UNPROD REARR
DSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	DHSGTGGGGSGSYF
VSAISGSGGSTYYADSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	KDNLWFD
AVISYDGSNKYYADSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	DLGGRGVVVVPAPGGRSIIYYGMDV
GAVISYDGSNKYYADSVKG	RFTISRDNKNSLYLQMSLRADDTAVYYCAR	LEGIGTIYYYGMDV
	AKNSLYLQMSLRADDTAVYYCVR	DDSSSWPKHFQ
QYAASTVKG	RFTISRDDSKNSLYLQMSLRADDTAVYYCVR	SGVVPYLDY

KNOWN FAMILY

AVYYCAR	DPRIARPDYYYYMDV
TAVYYCAR	GAEVVEFTARYYYGLNV

FIG. 11

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FR1	CDR1	FR2
YTTT	SYGDS	WVTTSPWTRCLRWMG
GEKPGSSVKV/SCKASGYTFT	DYFMN	WMRCAPGGRLEWMG
QVQLQETIGPRTEASETTLSTLCAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLQESGPGLVK*SETTSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
GYTFT	NYCMH	WVRQDHAQGLEWMG
QVQLQESGPGLVK*SETTSLYCAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
GPRLGEASETTLSTCTVSGGSIS	SSSYW	WIRQPPGKGLEWIG
QVQLQESGPGLVK*SETTSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
LSLCAVSGGSIS	SGNW*1	WVRQPPGKGLEWIG
SETTSLTCAVYGGSTF	GYIWS	WIRQPPGKGLEWIG
QVQLVQSGAEVKKPGASVKV/SCKASGYTFT	NYCMH	WVRQVLAQGLEWMG
SETTSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
SRAQTGEASETTLSTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
CPLTCTVSGGSVSSGS	YIWS	WIRQPPGKGLEWIG
GLVKPSETTSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
SETTSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSVKV/SCKASGYTFT	SYALS	WVRQAPGGGLEWMG
QVQLQESGPGLVK*SETTSLTCAVYGGSTF	GYIWS	WIRQPPGKGLEWIG
QVQLQESGPGLVK*SETTSLTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
GPGLVKPSETTSLTCTVSGGSIS	SGIYWS	WIRQPPGKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

FR1	FR2	CDR3
WISAYNGNTNYAQKLG	RVTMTDTSTSTAYMELSLRSEDATVYYCAR	DTVSS
WISAGNGNTKYSCKLG	RVTITRDTSTASTAYMQLSSLRSEDATVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
RIYTSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS
LVCPSDGSTSYAQKFGA	RVTITRDTSMSTAYMELSSLRSEDATVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS
LVCPSDGSTSYAQKFGA	RVTITRDTSMSTAYMELSSLRSEDATVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
SIYSGSTYYNPSLKS	RVTIPVDTSKNQFSLKLS*	
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS
RIYTSGSTNYNPSLKS	RVTMSVDTSKNQFSLKLS*	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
RIIPILGIANYAQKFG	RVTITADKSTSTAYMELSSLRSEDATVYYCAR	DTVS
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
YIYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS

FIG. 12

09722364-112800

12/23

pSW.

HindIII site AAGCTT

M K Y L L P T A A
 GCATGCAAAATTTCTATTTTCAAGGAGACAGTCATAATGAAATACCTATTGGCTACGGCAGCC
 10 20 30 40 50 60

A S L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTTTATTTACTGCTGCCCCAACCCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120

G F G L V A P S Q S L S I T C T V S G F
 GGACCTGGCTTGGTGGGCGCTTCCAGAGCGTGTCCATCAGATGCACCGCTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGTTATGGTGTAAATTTGGTTGCGCAGCGTCCAGGAAAGGTTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTTTGGGCTGATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACTCCAAAGAGCCAGTTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420

Q G T T V T V S S SmaI
 CAAGGCACCCAGGTCACCGTCTCTCTCATAATAAGAGCTATCCCGGCTAAGCTCGAATTC
 430 440 450 460 470 480

FIG. 13

pSW2

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HindIII AAGCTT

M K Y L L P T A A
GCATGCAAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60
A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCGCAACCAGCGATGGCCCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120
G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCGCTCACAGCGCTTCCATCAGATGCACCGTCTCAGGGTTC
130 140 150 160 170 180
S L T G Y G V N W V R Q P P G K G L E W
TCATTACCGCGCTATGCTGTAAGCTGGCTTGGCGAGCTCCAGGAAAGGGTCTGCAGTGG
190 200 210 220 230 240
L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGCGTGTATGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300
S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAGAGGCGAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360
D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCGGCTACTACTGTGCGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420
Q G T T V T V S S
CAAGGACCGCGCTCAGCGTCTCTCTCATTAATTAAGAGCTCGAATTCGCCAAGCTTGCATGC
430 440 450 460 470 480
M K Y L L P T A A A G
AAATTCCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCGCTGGA
490 500 510 520 530 540
L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCGCAACCAGCGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600
S L S A S V G E T V T I T C R A S G N I
TCCCTTTCTGCGTCTGTGGGAGAACTGTCAACATCACATGTGAGCAAGTGGGAATATT
610 620 630 640 650 660
H N Y L A W Y Q Q K Q G K S P Q L L V Y
CACAATTATTAGCATGGTATCAGCAGAAACAGGGAAATCTCTCTCAGTCTCTGGTCTAT
670 680 690 700 710 720

FIG. 14a

SUBSTITUTE SHEET

00321-4922260

14/23

Y T T T L A D G V P S R F S G S G S G T
 TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACA
 730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
 CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
 790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
 CATTTTGGAGTACTCCTCGGACCTTCGGTGGAGGCCACCAAGCTGGAATCAAACGGTAA
 850 860 870 880 890 900

TAAGAGCTCGAATTC
 910

FIG. 14 b

PSWHPOLYMYC

HindIII site AAGCTT

M K Y L L P T A A
 GCATGCAAAATTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
 70 80 90 100 110 PstI

Polylinker

TCTAGA GTCGAC CTCGAG
 XbaI SalI XhoI

MYC PEPTIDE

V T V S S E O K L I S E E D L N * *
 GGTCAACCTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
 BstEII

GGGCTAACCTCGAATTC

FIG. 15

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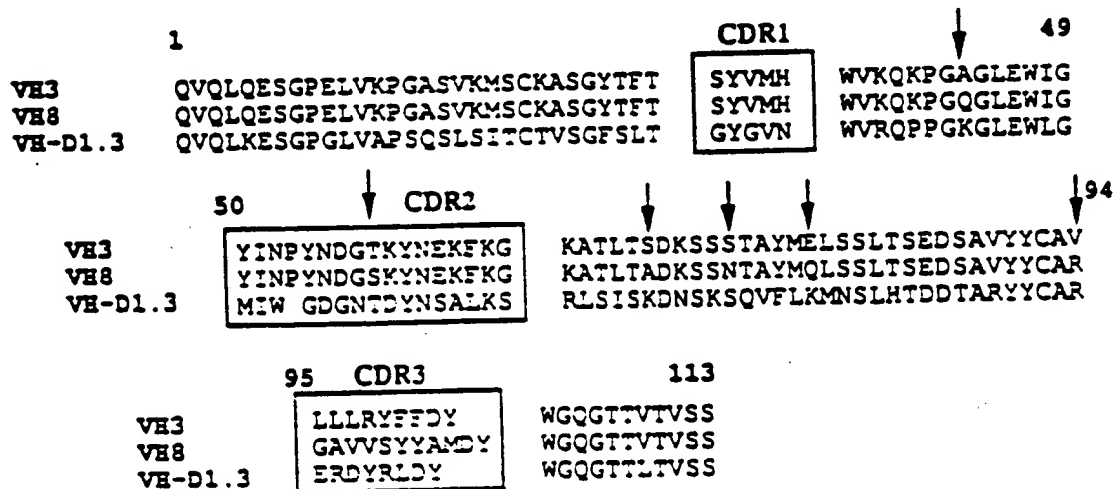


FIG. 16

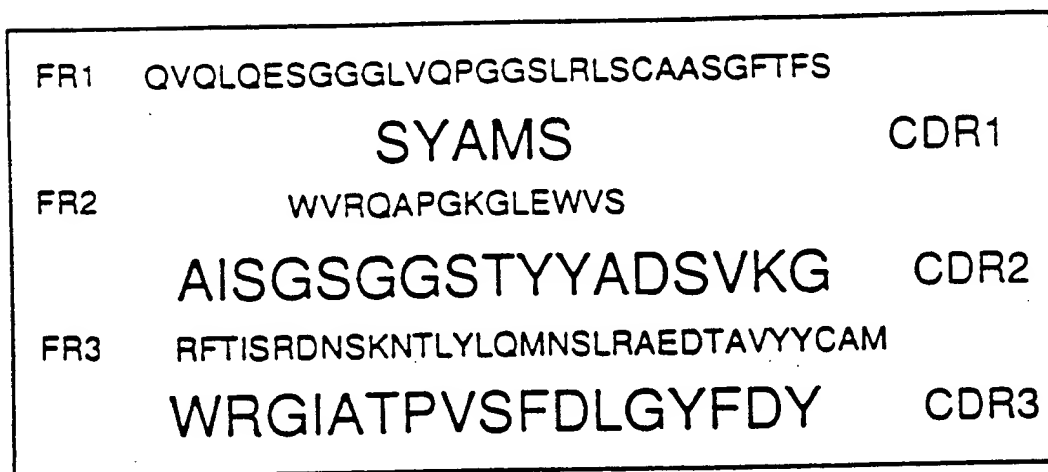


FIG. 17

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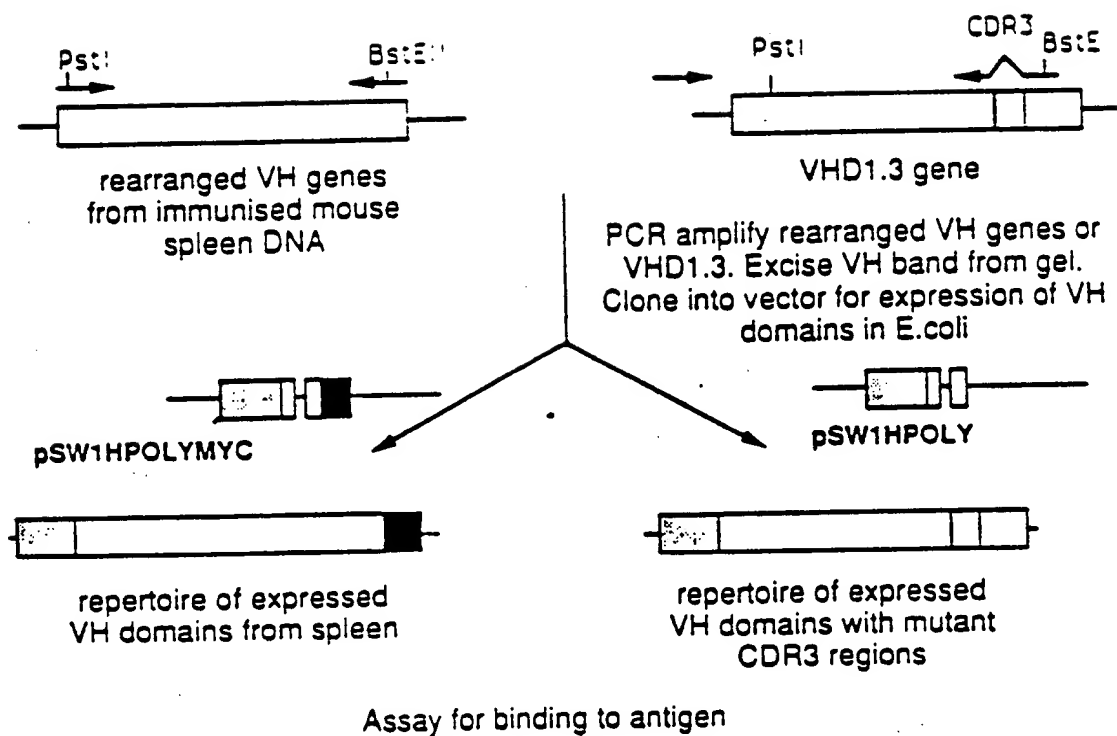


FIG. 18

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M K Y L L P T
AAGCTTGCATGCAAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG
10 20 30 40 50 60
A A A G L L L L A A Q P A M A Q V Q L Q
GCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAG
70 80 90 100 110 120
E S G P G L V A P S Q S L S I T C T V S
GAGTCAGGACCTGGCCTGGTGGCCGCTCACAGAGCCTGTCCATCACATGCACCGTCTCA
130 140 150 160 170 180
G F S L T G Y G V N W V R Q P P G K G L
GGGTTCTCATTAACCGGCTATGGTGAAACTGGGTTCCGAGCCTCCAGGAAGGGTCTG
190 200 210 220 230 240
E W L G M I W G D G N T D Y N S A L K S
GAGTGGCTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCC
250 260 270 280 290 300
R L S I S K D N S K S Q V F L K M N S L
AGACTGAGCATCAGCAAGGACAACTCCAGAGCCCAAGTTTCTTAAAAATGAACAGTCTG
310 320 330 340 350 360
H T C D T A R Y Y C A R E R D Y R L D Y
CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTAC
370 380 390 400 410 420
W G Q G T T V T V S S G G G A P A A A P
TGGGGCCAAAGGCCACCGGTCACCGTCTGCTCAGGTGGTGGTGGTCCAGCAGCTGCACCT
430 440 450 460 470 480
A G G G C V Q L K E S G P G L V A P S Q
GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCCTGGTGGCCGCTCACAG
490 500 510 520 530 540
S L S I T C T V S G F S L T G Y G V N W
AGCCTGTCCATCACATGCACCGTCTCAGGGTTCTCATTAACCGGCTATGGTGAAACTGG
550 560 570 580 590 600
V R Q P P G K G L E W L G M I W G D G N
GTTGCCAGCCCTCCAGGAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAC
610 620 630 640 650 660
T D Y N S A L K S R L S I S K D N S K S
ACAGACTATAATTCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGC
670 680 690 700 710 720
Q V F L K M N S L H T D D T A R Y Y C A
CAAGTTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC
730 740 750 760 770 780
R E R D Y R L D Y W G Q G T T V T V S S
AGAGAGAGAGATTATAGGCTTGACTACTGGGGCCAAAGGCACCGGTACCGTCTCTCTCA
790 800 810 820 830 840
TAATAAGAGCTC
850

FIG. 20

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FIG. 21 a

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FIG. 21c

[illegible]

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Q V Q L Q E S G P G L V Q P S Q S L S I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC
10 20 30 40 50 60

T C T V S G F S L T S Y G V H W V R Q S
ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCCGCCAGTCT
70 80 90 100 110 120

P G K G L E W L G M I W G D G N T D Y N
CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAAT
130 140 150 160 170 180

S A L K S R L S I S K D N S K S Q V F L
TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTA
190 200 210 220 230 240

K M N S L H T D D T A R Y Y C A R E R D
AAAATGAACAGTCTTSCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGAT
250 260 270 280 290 300

Y R L D Y W G Q G T T V T V S S
TATAGGCTTGACTACTGGGGCCAGGGGACCACGGTCACCGTCTCTCTCA
310 320 330 340

FIG. 23

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